



SEQUENCE LISTING

<110> Hornik, Vered

<120> CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOGS

<130> 87534-3000

<140> 09/734,583

<141> 2000-12-13

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 14

<212> PRT

<213> mammalian

<400> 1

Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
1 5 10

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> DISULFIDE BRIDGE

<222> (1)..(1)

<223> Cys residues at amino acid positions and 6 form a disulfide bridge

<220>

<221> MOD_RES
<222> (3)..(3)
<223> The Trp residue is the D isomer

<220>
<223> Synthetic peptide

<400> 2

Cys Phe Trp Lys Thr Cys
1 5

<210> 3
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N-Methyl

<220>
<221> MOD_RES
<222> (1)..(6)
<223> cyclo

<220>
<221> MOD_RES
<222> (3)..(3)
<223> The Trp residue is the D isomer
<220>
<223> Synthetic peptide

<400> 3

Ala Tyr Trp Lys Val Phe
1 5

<210> 4
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (1)..(1)
<223> The Phe residue is a D isomer

<220>
<221> MOD_RES
<222> (8)..(8)
<223> The Thr residue ends with CH2OH

<220>
<221> DISULFIDE BRIDGE
<222> (2)..(2)
<223> A disulfide bridge is formed between Cys residues 2 and 7

<220>
<221> MOD_RES
<222> (4)..(4)
<223> The Trp residue is a D isomer

<220>
<223> Synthetic peptide

<400> 4
Phe Cys Phe Trp Lys Thr Cys Thr
1 5

<210> 5
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<221> DISULFIDE

<222> (2)..(2)

<223> A Disulfide Bridge is formed between the Cys residues at position
2 and 6

<220>

<221> MOD_RES

<222> (1)..(1)

<223> The Phe residue is a D isomer

<220>

<221> MOD_RES

<222> (4)..(4)

<223> The Trp residue is a D isomer

<220>

<221> MOD_RES

<222> (7)..(7)

<223> The Thr residue ends with N2H

<220>

<223> Synthetic peptide

<400> 5

Phe Cys Phe Trp Lys Cys Thr
1 5

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> MISC_FEATURE
<222> (1)..(1)
<223> is a gamma amino butyric acid, diamino butyric acid, Gly, beta-Ala, 5-amino pentanoic acid or amino hexanoic acid; Residue 1 is bridged to Residue 8; Residue 1 also begins with a hydrogen, or a mono- or di- saccharide attached

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> is (D) or (L) Phe or Tyr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> is (D) or (L)-Trp, or (L)-Phe, (D)- or (L)-1Na1 or (D) or (L)-2Na1, or Tyr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> is (D) or (L)-Trp

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> is (D) or (L)-Lys

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> is Thr, Gly, Abu, Ser, Cys, Val, (D) or (L)-Ala, or (D)- or (L)-Ala, or Tyr

<220>
<221> MISC_FEATURE
<222> (7)..(7)

<223> is (D) or (L)-Phe, or (D)- or (L)-Ala, Nle, or Cys;

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> is Gly, Val, Leu, (D) or (L)-Phe, or 1NaI or 2NaI; with a terminal carboxy acid, amide or alcohol group.

<220>

<223> Synthetic peptide

<400> 6

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 7

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> is (D)- or (L)-Phe, or (D)- or (L)-Ala; wherein Residue 1 is bridged to Residue 6 a bridging group composed of 1 to 5 methyl spaces connected to an amide, thioether, thioester, or disulfide, followed by 1 to 5 methyl spacers

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> is Tyr or (D)- or (L)-Phe

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> is (D)- or (L)-Trp, (D)- or (L)-1NaI, or (D)- or (L)-2NaI

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> is Thr, Val, Ser, or Cys

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> is Gly or (D)- or (L)-Phe

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> is Thr, GABA, (D)- or (L)-1NaI, (D)- or (L)-2NaI, or (D)- or (L)-Phe

<220>

<223> synthetic peptide

<400> 7

Xaa Xaa Xaa Lys Xaa Xaa Xaa
1 5

<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> is absent or is a terminal group of four amino acids where some may be missing

<220>

<221> MISC_FEATURE

<222> (2)..(2)
<223> is 1Na1, 2Na1, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> may be absent, or are independently Gly, Tyr, 1Na1, 2Na1, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> (D)- or (L)-Trp

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> (D)- or (L)-Lys

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> is absent or is Gly, Abu, Cys, Thr, Val, (D)- or (L)-Ala, or (D)- or (L)-Phe

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> is Cys, (D)- or (L)-Ala, or (D)- or (L)-Phe

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> is absent or is Val, Thr, 1Na1 or 2Na1

<220>

<223> Synthetic peptide

<400> 8

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 9

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala; Residue 1 is connected to Residue 7 by a bridge comprised of 1 to 5 methylene spacers connected to an amide, thioether, thioester, or disulfide, followed by 1 to 5 methylene spacers

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> is absent or is (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> is (D)- or (L)-Tyr

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> is (D)- or (L)-Lys

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> is absent or is Thr, Val, Cys or (D)- or (L)-Ala

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> is a (D)- or (L)-Phe, Cys, or (D)- or (L)-Ala

<220>

<223> Synthetic peptide

<400> 9

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 10

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> is absent or is (D)- or (L)-Phe or Ala; the bridge is connected to Residue 1 or 2 and Residue 6 or 7, wherein the bridge is comprised of 1 to 5 methylene spacers connected to an amide, thioether, thioester, or disulfide, followed by 1 to 5 methylene spacers

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> is (D)- or (L)-Phe or Ala, Tyr

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> is (D)- or (L)-Trp

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> is (D)- or (L)-Lys

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> is Thr, Ala, Val, or Cys

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> is absent or is (D)- or (L)-Phe, Ala, or Cys

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> is absent or is Thr or Thr reduced to an alchoho1

<220>

<223> Synthetic peptide

<400> 10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5